

Align two sequences

Mon Mar 21 03:24:27 "GMT 2005

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/usr/tmp/seq1.100209.sca : 432 aa
>/usr/tmp/seq1.100209 [Unknown form], 432 bases, 432 aa vs.
>/usr/tmp/seq2.100209 [Unknown form], 446 bases, 446 aa
scoring matrix: , gap penalties: -12/-2
80.2% identity; Global alignment score: 2357

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019957-015920; SEQ ID NO: A
019957-019400; SEQ ID NO: 16

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      10      20      30      40      50
/usr/t MFQPLLDAPIESAPLKRWPLNLPP-LKIAVANWWGDEEIKKFKSVLYFILSQHYTTILH
      ..... .. : : .....
/usr/t MFQPLLDAYVESASIEKMASKSPPLKIAVANWWGDEEIKKFKSVLYFIFSQRYYTIALH
      10      20      30      40      50      60

      60      70      80      90      100     110
/usr/t RNPDKPADIVFGNPLGSARKILSYQNAKRIFYTGENEVPNPNLFDYAIGFDELDFRDRYL
      .....
/usr/t QNPNEFSDLVFSNPLGSARKILSYQNAKRIFYTGENEVPNPNLFDYAIGFDELDFRDRYL
      70      80      90      100     110     120

      120     130     140     150     160     170
/usr/t RMPLYYAYLHYKAEVNDTTSFYKLQPDLSYALKKPSHHFKENHPNLCVVNNESDPLKR
      .....
/usr/t RMPLYYDRLHHAESVNDTTSFYKLKDNLSLYTLKKPSHQFKENHPNLCVVNDESPLKR
      130     140     150     160     170     180

      180     190     200     210     220     230
/usr/t GFASFVANPNAPRRNAFYEALNAIEPVAGGGSVKNTLGYNVKNKSEFLSQYKFNLCFEN
      .....
/usr/t GVVSFVANANAPMRNAFYDALNSIEPVTGGGGSVKNTLGYNVKNKSEFLSQYKFNLCFEN
      190     200     210     220     230     240

      240     250     260     270     280     290
/usr/t TQGYGYVTEKIIDAYFSHTTIPIYWGSPSVAKDFNPKSFVNVHDFNMFDEAIDYIRYLHTH
      .....
/usr/t SQGYGYVTEKILDAYFSHTTIPIYWGSPSVAKDFNPKSFVNVHDFNMFDEAIDYIKYLHTH
      250     260     270     280     290     300

      300     310     320     330     340     350
/usr/t PNAYLDMHYENPLNTIDGKAYFYQNLSPKKILDFFKTIENDTIYHDNP--FIFYRDLNE
      .....
/usr/t PNAYLDMHYENPLNLDGKAYFYQDLSPKKILAFFKTIENDTIYHKSSTSFMWECDLDE
      310     320     330     340     350     360

      360     370     380     390     400
/usr/t PSVSIIDGLRVNYDDLVRVNYDDLVRVNY-----ERLLQNASPLLEL
      .....
/usr/t PLASIDDLRVNYDDLVRVNYDDLVRVNYDDLVRVNYDDLVRVNYERLLQNASPLLEL
      370     380     390     400     410     420

      410     420     430
/usr/t SQNTTFKIKYRKAYQKSLPLLRAIRRWVKK
      .....
/usr/t SQNTSFKIKYRKAYQK--PI-KNPYPYCAP
      430     440

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Elapsed time: 0:00:00

Exhibit A